WHAT IS CLAIMED IS:

1. A method of nucleic acid sequencing comprising the steps:

(a) amplifying a nucleic acid sample to produce an amplified DNA product;

(b) extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products;

(c) detecting a total amount of label present in the collection to produce a measurement; and

(d) combining a plurality of measurements to determine DNA sequence information about the sample.

2. A method as described in Claim 1 wherein each measurement of a label corresponds to an amount of terminating nucleotide.

3. A method as described in Claim 1 wherein the DNA sequence information corresponds to a length of the DNA sequence.

4. A method as described in Claim 1 wherein the DNA sequence information corresponds to a plurality of bases in the DNA sequence.

5. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for human identification.

6. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for diagnostic testing.

7. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for genetic localization or gene discovery.

8. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for criminal justice applications.

9. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used in conjunction with a DNA database of genetic polymorphisms.

10. A method as described in Claim 1, wherein after the combining step, the DNA sequence information is used for cancer assessment.

11. A system for nucleic acid sequencing comprising:

(a) a means for amplifying a nucleic acid sample to produce an amplified nucleic acid product;

(b) a means for extending a sequencing primer bound to the DNA product in the presence of terminating nucleotide analogs to produce a collection of labeled nucleic acid products, said extending means in connection with the amplified product;

(c) a means for detecting a total amount of label present in the collection to produce a measurement, said detecting means in connection with the collection; and

(d) a means for combining a plurality of measurements to determine DNA sequence information about the sample, said combining means in connection with the measurement.

12. A system as described in Claim 11, wherein the amplifying means includes a PCR thermocycler, the extending means includes a chamber that permits DNA sequencing reactions to occur in the presence of terminating nucleotide analogs, the detecting means measures fluorescent or other labels that quantify an amount of DNA molecules, and the combining means includes a computing device with memory.

13. A method for obtaining information about a signal comprising the steps:

(a) inducing a decay function;

(b) imposing the decay function on a signal;

(c) forming a numerical quantity that characterizes the signal's behavior in the presence of the decay function;

(d) combining a plurity of such numerical quantities to obtain information about the signal.

14. A method as described in Claim 13 wherein the signal is a nucleic acid sequence, the decay function is induced by introducing dideoxy terminator analogs into a sequencing reaction, the numerical quantities correspond to Laplace transform coefficients, and the obtained information helps characterize the sequence.

15. A method as described in Claim 14 wherein the characterization does not completely describe the nucleic acid sequence.

16. A method as described in Claim 15 wherein the incomplete sequence information describes a genetic polymorphism.